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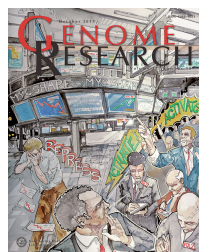
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Corrigendum: A comparative analysis of whole genome sequencing of esophageal adenocarcinoma pre- and post-chemotherapy 1782

Ayesha Noorani, Jan Bornschein, Andy G. Lynch, Maria Secrier, Achilleas Achilleos, Matthew Eldridge, Lawrence Bower, Jamie M.J. Weaver, Jason Crawte, Chin-Ann Ong, Nicholas Shannon, Shona MacRae, Nicola Grehan, Barbara Nutzinger, Maria O'Donovan, Richard Hardwick, Simon Tavaré, Rebecca C. Fitzgerald, on behalf of the Oesophageal Cancer Clinical and Molecular Stratification (OCCAMS) Consortium

^{OA}Open Access paper



Cover The MYC transcription factor and proto-oncogene controls fundamental biological processes and is present at high levels in numerous cancer types. Despite its relevance, it is still unclear how increased levels of MYC could activate or repress specific sets of target genes. In this study, the change in the proportion of MYC binding (the MYC share) is revealed to promote a corresponding variation in the recruitment of RNAPII (Pol2), thus determining the sign of the transcriptional response of the downstream gene. The cover depicts a number of stockbrokers, each representing a Pol2 complex, which in response to the surge of the MYC share (green upward trend in the stock exchange monitor), crowd and invoke the “transcriptional” activation (also depicted as the act of transcribing on paper). On the left side, a lonely stockbroker desperately reacts to the fall of the MYC share (red downward trend in the monitor and in the falling sheets of paper) by lamenting the “transcriptional” repression. (Cover illustration by Andrea Kiv Marrapodi, <http://www.kiv-art.it>. [For details, see de Pretis et al., pp. 1658–1664.]